Appl. No. 10/087,541
Response to Restriction Requirement dated April 25, 2005
Reply to Office Action of March 24, 2005

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1.   (Withdrawn) A method for comparing a query peptide to a plurality of database peptides comprising the steps of:

(a)   constructing an index table, said index table comprising a plurality of records corresponding to a plurality of allowed mass values, said records comprising zero or more fields, said constructing step comprising the steps of:

(i)   selecting a first peptide from said plurality of database peptides;

(ii)   calculating a plurality of associated masses for said first peptide;

(iii)   selecting a first associated mass from said plurality of associated masses;

(iv)   referencing a first record from said plurality of records, said first record corresponding to said first associated mass;

(v)   entering a first field into said first record, said first field comprising a first peptide index referencing said first peptide;

(vi)   repeating steps (iii)-(v) for at least one other associated mass from said plurality of associated masses;

(vii)   repeating steps (i)-(vi) for at least one other peptide from said plurality of database peptides; and

(b)   generating a plurality of comparison scores, said plurality of comparison scores corresponding to said plurality of database peptides, said generating step comprising the steps of:

(i)   generating a plurality of query mass values for said query peptide;

(ii)   selecting a first query mass value from said plurality of query mass values;

(iii)   referencing a second record from said plurality of records, said second record corresponding to said first query mass value;

(iv)   selecting a second field from said second record, said second field comprising a second peptide index;

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      (v)   selecting a first comparison score from said plurality of comparison scores, said first comparison score corresponding to said second peptide index;

      (vi)   incrementing said first comparison score;

      (vii)   repeating steps (ii)-(vi) for at least one other query mass value selected from said plurality of query mass values.

2.   (Withdrawn) The method of claim 1 wherein said generating step (b)(i) comprises the step of performing mass spectroscopy on said query peptide.

3.   (Withdrawn) The method of claim 2 wherein said mass spectroscopy is performed by a method selected from the set consisting of: Fourier transform ion cyclotron resonance ("FTICR"), quadrupole mass spectroscopy, ion trap mass spectroscopy, and time-of-flight mass spectroscopy.

4.   (Withdrawn) The method of claim 1 wherein said calculating step (a)(ii) comprises the step of calculating a plurality of associated masses for said first peptide, said plurality of associate masses comprising a plurality of primary masses and a plurality of complementary masses.

5.   (Withdrawn) The method of claim 1 wherein said generating step (b) further comprises the step of multiplying said first comparison score by a weight value, wherein said weight value is a function of the type of mass value.

6.   (Withdrawn) The method of claim 5 wherein said type of mass value is selected from the group consisting of: y-ion, b-ion, peak mass, and complementary mass.

7.   (Withdrawn) A method for comparing a query peptide to a plurality of database peptides comprising the steps of:

      (a)   constructing a first index table, said first index table comprising a first plurality of records corresponding to a plurality of allowed mass values, said records comprising zero or more fields; and

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(b)   constructing a second index table, said second index table comprising a second plurality of records corresponding to said plurality of allowed mass values, said records comprising zero or more fields; and

(c)   calculating a plurality weight values, said weight values set according to the predictive value of said first and second index tables.

8.   (Amended) A method for comparing a modified query peptide to a plurality of database peptides comprising the steps of:

(a)   generating a plurality of query mass values for said <u>modified</u> query peptide;

(b)   identifying a set of [query] <u>modified</u> mass values from said plurality of query mass values[, wherein said set corresponds to modified mass values];

(c)   determining a spectral range for said <u>modified</u> query peptide;

(d)   subdividing said spectral range into a plurality of <u>mass</u> [equal] intervals; and

(e)   performing a plurality of searches on said plurality of <u>mass</u> [equal] intervals <u>comparing the modified query peptide to the plurality of database peptides.</u>

9.   (Amended) The method of claim 8 further comprising the step of excluding said [set of query] <u>modified</u> mass values <u>during the comparison of the modified query peptide to the plurality of database peptides</u>.

10.   (Amended) The method of claim 8 further comprising the step of adjusting said [set of query] <u>modified</u> mass values <u>during the comparison of the modified query peptide to the plurality of database peptides</u>.

11.   (Withdrawn) A method for comparing a query peptide to a plurality of database peptides comprising the step of constructing an index table, said index table comprising a plurality of records corresponding to a plurality of allowed mass values, said records comprising zero or more fields, said constructing step comprising the steps of:

(i)   selecting a first peptide from said plurality of database peptides;

(ii)   identifying a modification site on said first peptide;

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(iii)   applying a modification to said modification site, producing a first modified peptide;

(iv)   calculating a plurality of associated masses for said first modified peptide;

(v)   selecting a first associated mass from said plurality of associated masses;

(vi)   referencing a first record from said plurality of records, said first record corresponding to said first associated mass;

(vii)   entering a first field into said first record, said first field comprising a first peptide index referencing said first peptide;

(viii)   repeating steps (v)-(vii) for at least one other associated mass from said plurality of associated masses;

(ix)   repeating steps (i)-(viii) for at least one other peptide from said plurality of database peptides.

12.   (Amended) The method of claim [11] 8 wherein [said identification step (ii) comprises the step of identifying] the modified mass value corresponds to a modification site selected from the group consisting of: a phosphorylation site, an oxidation site, and a substitution site.

13.   (Original) The method of claim 12 wherein said phosphorylation site comprises an amino acid selected from the group consisting of: serine, threonine, and tyrosine.

14.   (Original) The method of claim 12 wherein said oxidation site comprises an amino acid selected from the group consisting of: cysteine and methionine.

15.   (Original) The method of claim 12 wherein said substitution site comprises an amino acid selected from the group consisting of: glutamine, glutamate, asparagine, and aspartate.

16.   (New) The method of claim 8 wherein the spectral range of the modified query peptide has a value from zero to the unmodified query peptides mass.

17.   (New) The method of claim 8 wherein a selected comparison between the modified query peptide and the plurality of database peptides further identifies modified mass values for

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the modified query peptide that reside within the mass interval of the selected comparison.

18. (New) The method of claim 8 further comprising collectively evaluating the comparisons of the modified query peptide to the plurality of database peptides to identify a best match between the modified query peptide and the plurality of database peptides.

19. (New) The method of claim 8 further comprising collectively evaluating the comparisons of the modified query peptide to the plurality of database peptides to determine the putative identity of the modified query peptide.